

SEQUENCE LISTING

<110> National Institute of Advanced Industrial Science and Technology

<120> A GDP-4-keto-6-deoxy-D-mannose-3,5-epimerase-4-reductase
Gene From Arabidopsis Thaliana and Method for Producing
A GDP-fucose Using Thereof

<130> PH-935-PCT

<150> JP 11-329045

<151> 1999-11-19

<160> 6

<170> PatentIn Ver. 2.0

<210> 1

<211> 312

<212> PRT

<213> Arabidopsis thaliana

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30

Leu Val Leu Lys Thr His Ala Glu Leu Asp Leu Thr Arg Gln Ala Asp
 35 40 45

Val Glu Ser Phe Phe Ser Gln Glu Lys Pro Val Tyr Val Ile Leu Ala
 50 55 60

Ala Ala Lys Val Gly Gly Ile His Ala Asn Asn Thr Tyr Pro Ala Asp
 65 70 75 80

Phe Ile Gly Val Asn Leu Gln Ile Gln Thr Asn Val Ile His Ser Ala
 85 90 95

Tyr Glu His Gly Val Lys Lys Leu Leu Phe Leu Gly Ser Ser Cys Ile
 100 105 110

Tyr Pro Lys Phe Ala Pro Gln Pro Ile Pro Glu Ser Ala Leu Leu Thr
 115 120 125

Ala Ser Leu Glu Pro Thr Asn Glu Trp Tyr Ala Ile Ala Lys Ile Ala
 130 135 140

Gly Ile Lys Thr Cys Gln Ala Tyr Arg Ile Gln His Gly Trp Asp Ala
 145 150 155 160

Ile Ser Gly Met Pro Thr Asn Leu Tyr Gly Pro Asn Asp Asn Phe His
 165 170 175

Pro Glu Asn Ser His Val Leu Pro Ala Leu Met Arg Arg Phe His Glu
 180 185 190

Ala Lys Val Asn Gly Ala Glu Glu Val Val Val Trp Gly Thr Gly Ser
 195 200 205

Pro Leu Arg Glu Phe Leu His Val Asp Asp Leu Ala Asp Ala Cys Val
 210 215 220

Phe Leu Leu Asp Arg Tyr Ser Gly Leu Glu His Val Asn Ile Gly Ser
 225 230 235 240

Gly Gln Glu Val Thr Ile Arg Glu Leu Ala Glu Leu Val Lys Glu Val
 245 250 255

Val Gly Phe Glu Gly Lys Leu Gly Trp Asp Cys Thr Lys Pro Asp Gly
 260 265 270

Thr Pro Arg Lys Leu Met Asp Ser Ser Lys Leu Ala Ser Leu Gly Trp
 275 280 285

Thr Pro Lys Val Ser Leu Arg Asp Gly Leu Ser Gln Thr Tyr Asp Trp
 290 295 300

Tyr Leu Lys Asn Val Cys Asn Arg
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<213> Arabidopsis thaliana

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gtt gga tct gcc att gtc cgc aag ctt cag gaa caa ggt ttc acc aat 96
Val Gly Ser Ala Ile Val Arg Lys Leu Gln Glu Gln Gly Phe Thr Asn
20 25 30

ctc gtt ctt aaa aca cac gcc gag ctt gat ctc act cgt caa gcc gat 144
Leu Val Leu Lys Thr His Ala Glu Leu Asp Leu Thr Arg Gln Ala Asp
35 40 45

gtt gaa tcc ttc ttt tct caa gag aag cca gtt tat gta atc cta gca 192
Val Glu Ser Phe Phe Ser Gln Glu Lys Pro Val Tyr Val Ile Leu Ala
50 55 60

gca gct aaa gtt ggt ggt att cac gct aac aac acc tat cct gct gat 240
Ala Ala Lys Val Gly Gly Ile His Ala Asn Asn Thr Tyr Pro Ala Asp
65 70 75 80

ttc att ggt gtc aat ctc cag att cag acc aat gtg atc cac tct gca 288
Phe Ile Gly Val Asn Leu Gln Ile Gln Thr Asn Val Ile His Ser Ala

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90

95

tat gag cac ggt gtg aag aag ctt ctc ttc ctt gga tca tcc tgc att 336

Tyr Glu His Gly Val Lys Lys Leu Leu Phe Leu Gly Ser Ser Cys Ile

100

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110

tac cct aaa ttt gct cct cag cca att cct gag tct gct ttg tta aca 384

Tyr Pro Lys Phe Ala Pro Gln Pro Ile Pro Glu Ser Ala Leu Leu Thr

115

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gca tcg ctt gaa cca act aat gag tgg tat gct att gct aag atc gct 432

Ala Ser Leu Glu Pro Thr Asn Glu Trp Tyr Ala Ile Ala Lys Ile Ala

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ggg att aag act tgt cag gct tat agg att cag cac gga tgg gat gca 480

Gly Ile Lys Thr Cys Gln Ala Tyr Arg Ile Gln His Gly Trp Asp Ala

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atc tct ggc atg cct act aat ctc tat ggt cct aat gac aat ttc cac 528

Ile Ser Gly Met Pro Thr Asn Leu Tyr Gly Pro Asn Asp Asn Phe His

165

170

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ccg gag aat tct cat gtg ctt cct gct ctt atg agg agg ttc cac gag 576

Pro Glu Asn Ser His Val Leu Pro Ala Leu Met Arg Arg Phe His Glu

180

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190

gcg aaa gtg aat gga gcg gag gaa gtt gtg gtg tgg ggt aca ggt agt 624

Ala Lys Val Asn Gly Ala Glu Glu Val Val Val Trp Gly Thr Gly Ser

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ccg ttg agg gag ttc ttg cat gtt gat gat ttg gct gat gct tgt gtt 672
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210

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Phe Leu Leu Asp Arg Tyr Ser Gly Leu Glu His Val Asn Ile Gly Ser

225

230

235

240

ggt caa gaa gtg act att aga gag ttg gct gag ttg gtg aaa gag gtt 768

Gly Gln Glu Val Thr Ile Arg Glu Leu Ala Glu Leu Val Lys Glu Val

245

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gtt ggt ttt gaa ggg aag ctt gga tgg gat tgc act aag cca gat ggc 816

Val Gly Phe Glu Gly Lys Leu Gly Trp Asp Cys Thr Lys Pro Asp Gly

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aca ccg agg aaa ctt atg gac agc tca aag ctc gcg tct ttg ggt tgg 864

Thr Pro Arg Lys Leu Met Asp Ser Ser Lys Leu Ala Ser Leu Gly Trp

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aca cct aag gtt tct ctt aga gat ggt ctg agc caa act tat gat tgg 912

Thr Pro Lys Val Ser Leu Arg Asp Gly Leu Ser Gln Thr Tyr Asp Trp

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Tyr Leu Lys Asn Val Cys Asn Arg

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<213> Artificial Sequence

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<223> Description of Artificial Sequence:Primer

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<213> Artificial Sequence

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<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:Primer

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<210> 6

<211> 27

<212> DNA

<213> Artificial Sequence

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27